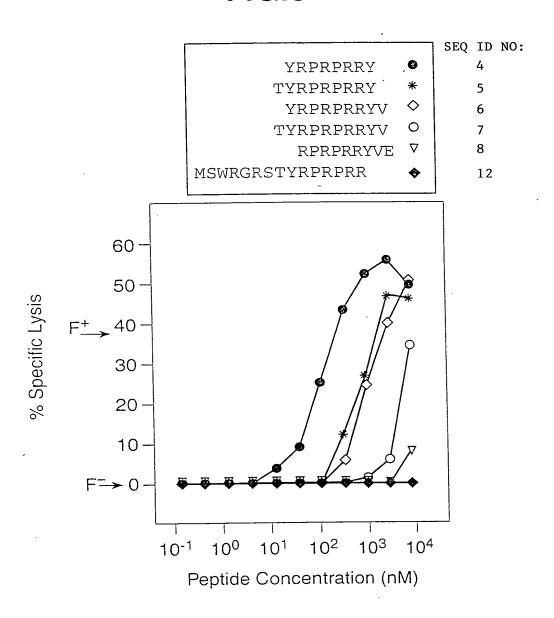


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FIG.3





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SEQ

TACTGAGATTCA TACTGAGATTCA SCCAACTCATAT TACTGAGATTCA TACTGAGATTCA TACTGAGATTCA	
CCGGACTCTTTTTCCTCTAGGGCGCTCTTTTTCCTCTCTCT	
ACGCCAGGGAG CTGTGAGGCAGTGCTGTGTGCTTCCTGCCG TCCGGACTCTTTTTCCTGTACTGAGATTCA ACGCCAGGGAG AAGATCGACCTATTATTGGTCTAGGCCAAT AATAGGTCGATTTTTCCTGGCCAACTCATAT AGATGAGTTGGCGAGG AAGATCGACCTATTATTGGTCTAGGCCAAT AATAGGTCGATGTTCCTGCCAACTCATATCGCCAGGGAG CTGTGAGGCAGTGCTGTGGTTCCTGCCG TCCGGACTCTTTTTCCTGTACTGAGATTCAAG CTGTGAGGCAGTGCTGTGGTTCCTGCCG TCCGGACTCTTTTTCCTGTACTGAGATTCA	
CTCATATITCACACAGATGGGAG CTGTGAGGCAGTGCTGTGTGGGTTCCTGCCG TCCGGACTCTTTTTTCCTGTACTGAGATTCA CTCATATITCACACAGATGGGAGG AAGATCGACCTATTATTGGTCTAGGCCAAT AATAGGTCGATGTTCCTGGCCAACTCATAT CTCATATITCACACAGAGGGGGGGGGGGGGGGGGGGGGGG	
ID NO: 01 GAGE-1 14 GAGE-2 15 GAGE-3 16 GAGE-4 17 GAGE-5 18 GAGE-6	

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AGC AGC AGC AGC
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) GA(
TCTGTGTGAAATATGAGTTGGGGAGGAAGA TCGACGTATGGGCCTAGACCAAGACGC TAGGTAGAGCCTCCTGAAATGATTGGGCCT 1 TCTGTGTGAAATATGAGTTGGGGAAGAA TCGACGTATGGCCTAGACCAAGGCGC TAGGTAGAGCCTCCTGAAATGATTGGGCCT 1 TTCACACAGATGAATGTGAGAGAAAA TCGACGTATTATTGGCCTAGACCAAGGCGC TATGTAGAGCCTCCTGAAATGATTGGGCCT 1 TCTGTGTGAAATATGAGTTGGCGAGGAAGA TCGACGTATTATTGGCCTAGACCAAGGCGC TATGTAGAGCCTCCTGAAATGATTGGGCCT 1 TCTGTGTGAAATATGAGTTGGCGAGGAAGA TCGACGTATTATTGGCCTAGACCAAGGCGC TATGTAGAGCCTCCTGAAGTGATTGGGCCT 1 TCTGTGTGAAATATGAGTTGGCGAGGAAGA TCGACGTATTATTGGCCTAGACCAAGGCGC TATGTAGAGCCTCCTGAAGTGATTGGGCCT 1
A A A A A A
GAI GAI GAI GAI
SAG SAG SAG SAG SAG
TTC TTC CAG TTC TTC
AAG PAG PAG PAG
(TATATATATATATATATATATATATATATATATATATA
AATI AAT AAT AAT
16A 16A 16A 16A
TGT CAC TGT TGT
CTG CTG CTG CTG
E 01 GAGE-1 E 14 GAGE-2 E 15 GAGE-3 E 16 GAGE-4 E 17 GAGE-5 E 18 GAGE-6
01 GAGE-1 14 GAGE-2 15 GAGE-3 16 GAGE-4 17 GAGE-5 18 GAGE-6
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Ų	-5 ATGUEGUULGAGUAGIIUAGIIGAAGIAGAAGIA GAAGUAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	出てて出ててるでである。
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٥	-6 ATGCGGCCCGAGCAGTTCAGTGATGAAGTG GAACCAAGTGCTGTGCT	
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CAGGAACAGGGTCACCCACAGACTGGGTGT CAGGAACAGGGTCACCCACAGACTGGGTGT CAGGAACAGGGTCACCCACAGACTGGGTGT CAGGAACAGGGTCACCCACAGACTGGGTGT CAGGAACAGGGTCACCACAGACTGGGTGT CAGGAACAGGGTCACCCACAGACTGGGTGT GGTCAAGGGCCGAAGCCTGAAGCTAATAGC **GGTCAAGGGCCGAAGCCTGAAGCTIGATAGC** GGTCAAGGGCCGAAGCCTGAAGCT|QATAGC GGTCAAGGGCCGAAGCCTGAAGCTGATAGC GGTCAAGGGCCGAAGCCTGAAGCTAATAGC GGTCAAGGGCCGAAGCCTGAAGCTKATAGC CAGGAGGAGGATGAGGGAGCATCTGCA CAGGAGGAGGATGAGGGAGCATCTGCA CAGGAGGAGAGGATGAGGGAGCATCTGCA CAGGAGGAGGATGAGGGAGCATCTGCA CAGGAGGAGGATGAGGGAGCATCTGCA CAGGAGGAGAGGATGAGGGAGCATCTGCA 18 GAGE-6 16 GAGE-4 17 GAGE-5 15 GAGE-3 14 GAGE-2 01 GAGE-1

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FIG. 4B

84444	444444	5 4 4 4 4	22222
ACGCCTGAAGAAGAGATGAGGTCTCACTAT ACGCCTGAAGAAG	CGGAAACCTTGAGTGACTGAAATATCAAAT	AGAAGACATGCTGAAATGTTGCAGGCTGCT AGAAGACACGTTGAAATGATGCAGGCTGCT AGAAGGCACGTTGAAATGATGCAGGCTGCT AGAAGGCACGTTGAAATGATGCAGGCTGCT AGAAGGCACGTTGAAATGATGCAGGCTGCT AGAAGACACGTTTGAAATGATGCAGGCTGCT	GAAAAAAAAAA GAAAAAAAAAA GAAAAAAAAAAA AAAAAA
ATGGACCCGCCAAATCCAGAGGAGGTGAAA ATGGACCCGCCAAATCCAGAGGAGGTGAAA ATGGACCCGCCAAATCCAGAGGAGGTGAAA ATGGACCCGCCAAATCCAGAGGAGGTGAAA ATGGACCCGCCAAATCCAGAGGAGGTGAAA	ATGAACAATTGCTTCTTAAATCTTTCCCCA	TGGCATGTGAAGGGCAATCACAGTGTTAAAGTGAAAAGCAATCACAGTGTTAAAGTGAAAAGCAATCACAGTGTTAAAGTGAAAAGCAATCACAGTGTTAAAGTGAAAAGCAATCACAGTGTTAAA	TCCCAATAAAGCTTTACAGCCTTCTGCAAA TCCCAATAAAGCTTTACAGCCTTCTGCAAA TCCCAATAAAGCTTTACAGCCTTCTGCAAA TCCCAATAAAGCTTTACAGCCTTCTGCAAA
VDE 24 GAGTGTGAAGATGGTCCTGATGGGCAGGAG GAGTGTGAAGATGGTCCTGATGGGCAGGAG GAGTGTGAAGATGGTCCTGATGGGCAGGAG GAGTGTGAAGATGGTCCTGATGGGCAGGAG GAGTGTGAAGATGGTCCTGATGGGCAGGAG GAGTGTGAAGATGGTCCTGATGGGCAGGAG	GTTGCCCAGACTGGGATTCTCTGGCTTTTA	GGCGAGACCGTTTAGTTTCCTATCATCTG	CCTATGTTGGAAAITTCTTTCATTIGAAGITTCCTTCATTIAAAAITTCCTCCTATGTTGGAAAITTTGTTCATTIAAAAITTCCTCCTTIAAAAITTCCTTATTCATTIAAAAITTCCCTATGTTTGGAAAITTTGTTTCATTIAAAAITTCCCTATGTTTGGAAAITTTGTTTCATTIAAAAITTCCCTATGTTTGGAAAITTTGTTTCATTIAAAAITTCCCTATGTTTGGAAAITTTGTTTCATTIAAAAAITTCCCTATGTTTGGAAAITTTGTTTCATTIAAAAITTC
nt of 01GAGE-1 nt of 14GAGE-2 nt of 15GAGE-3 nt of 16GAGE-4 nt of 17GAGE-5 nt of 18GAGE-6	nt of 01 GAGE-1 nt of 14 GAGE-2 nt of 15 GAGE-3 nt of 17 GAGE-5 nt of 17 GAGE-5	of of of	nt of 01 GAGE-1 nt of 14 GAGE-2 nt of 15 GAGE-3 nt of 16 GAGE-4 nt of 17 GAGE-5 nt of 18 GAGE-6

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FIG. 5

PEA PEA PEA PEA PEA	
RQDPAAAQEGEDEGASAGQGPK RQDPAAAQEGEDEGASAGQGPK RQDPAAAQEGEDEGASAGQGPK RQDPAAAQEGEDEGASAGQGPK RQDPAAAQEGEDEGASAGQGPK RQDPAAAQEGEDEGASAGQGPK	LLMNNCFLMLSPRKP
Antigenic Peptide	SQEQGHPQTGCECEDGPDGQEMDP PNPEEVKTPEEEMRSHYVAQTGILM HSQEQGHPQTGCECEDGPDGQEMDP PNPEEVKTPEEGEKQSQC
MS-WRGRST MNLSMGRST MNLSMGRST MS-WRGRST MS-WRGRST MS-WRGRST	DSQEQGHPQTGCECEDGPDGQEMDP PNPEEVKTPEEEMRSHYVAQTGILM LLMNNCFLMLSPRKPHSQEQGHPQTGCECEDGPDGQEMDP PNPEEVKTPEEGEKQSQC
SEQ ID NO: 26 GAGE-1 27 GAGE-2 28 GAGE-3 29 GAGE-4 30 GAGE-5 31 GAGE-5	nt of 26GAGE-1 nt of 27GAGE-2 nt of 28GAGE-3 nt of 29GAGE-4

DSQEQGHPQTGCECEDGPDGQEMDP PNPEEVKTPEEGEKQSQC---

nt of 30GAGE-5 nt of 31GAGE-6



FIG. 6

